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Simulating Dengue: Comparison of Observed and Predicted Cases from Generic Reaction-Diffusion Model for Transmission of Mosquito-Borne Diseases

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Abstract Dengue is a mosquito-borne disease caused by virus and found mostly in urban and semi-urban areas, in many regions of the world. Female aedes mosquitoes, which usually bite during daytime, spread the disease. This flu-like disease may progress to severe dengue and cause fatality. A generic reaction-diffusion model for transmission of mosquito-borne diseases was proposed and formulated. The motivation is to explore the ability of the generic model to reproduce observed dengue cases in Borneo, Malaysia. Dengue prevalence in four districts in Borneo namely Kuching, Sibu, Bintulu and Miri are compared with simulations results obtained from the temporal and spatio-temporal generic model respectively. Random diffusion of human and mosquito populations are taken into account in the spatio-temporal model. It is found that temporal simulations closely resemble the general behavior of actual prevalence in the three locations except for Bintulu. The recovery rate in Bintulu district is found to be the lowest among the districts, suggesting a different dengue serotype may be present. From observation, the temporal generic model underestimates the recovery rate in comparison to the spatio-temporal generic model.

Keywords Mosquito-borne, dengue, transmission, generic, model

Mathematics Subject Classification 35E15, 37M05

1 Introduction

Dengue incidences have developed tremendously over the years. According to World Health Organization [1], the number of dengue cases reported increased from 2.2 million in 2010 to 3.2